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RAW SEQUENCE LISTING

DATE: 09/29/2004

PATENT APPLICATION:, US/10/729,571B

TIME: 11:56:16

Input Set : A:\ASZD-P01-007.TXT

Output Set: N:\CRF4\09292004\J729571B.raw

4 <110> APPLICANT: Anderson, Marie
 5 Fisher, Stewart
 6 Folmer, Rutger Henk
 7 Kern, Gunther
 8 Lundquvist, Rolf T.
 9 Newton, David Trevor
 10 Xue, Yafeng
 12 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF GLUTAMATE RACEMASE
 13 (MURI)
 15 <130> FILE REFERENCE: ASZD-P01-007
 17 <140> CURRENT APPLICATION NUMBER: US 10/729,571B
 18 <141> CURRENT FILING DATE: 2003-12-05
 20 <150> PRIOR APPLICATION NUMBER: US 60/435,167
 21 <151> PRIOR FILING DATE: 2002-12-20
 23 <150> PRIOR APPLICATION NUMBER: US 60/435,272
 24 <151> PRIOR FILING DATE: 2002-12-20
 26 <150> PRIOR APPLICATION NUMBER: US 60/435,527
 27 <151> PRIOR FILING DATE: 2002-12-20
 29 <160> NUMBER OF SEQ ID NOS: 76
 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 35 <212> TYPE: DNA
 36 <213> ORGANISM: H. pylori
 38 <220> FEATURE:
 39 <221> NAME/KEY: CDS
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 45 1 5 10 15
 47 aaa agc ctt tta aaa gcg cga ttg ttt gat gaa atc atc tac tat ggc 96
 48 Lys Ser Leu Leu Lys Ala Arg Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
 49 20 25 30
 51 gat agc gct aga gtg cct tat ggc act aaa gac ccc acc acg atc aag 144
 52 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
 53 35 40 45
 55 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cat gag att gaa 192
 56 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu
 57 50 55 60
 59 tta ttg att gtg gca tgc aac acc gcg agc gct ctg gct tta gaa gag 240
 60 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
 61 65 70 75 80

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63 atg caa aag tat tct aaa atc cct att gtg ggc gtg att gag cca agc 288
64 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
65      85      90      95
67 att tta gcg atc aag cgg caa gtg gaa gat aaa aac gcc cct att tta 336
68 Ile Leu Ala Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu
69      100      105      110
71 gtg cta ggg aca aaa gcg acg att caa tcc aac gcc tat gac aac gcc 384
72 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
73      115      120      125
75 ctg aaa caa caa ggc tat ttg aac att tcg cat tta gct act tct ctt 432
76 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
77      130      135      140
79 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gaa 480
80 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
81 145      150      155      160
83 act tgc atg cat tat tat ttc act ccc tta gag att tta ccc gaa gtg 528
84 Thr Cys Met His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
85      165      170      175
87 atc att tta ggt tgc acg cat ttt ccc tta atc gct caa aaa att gag 576
88 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
89      180      185      190
91 ggc tat ttc atg ggg cat ttt gcc ctt cca acg ccc ccc cta ctc atc 624
92 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
93      195      200      205
95 cat tcg ggc gat gct att gta gaa tat ttg caa caa aaa tac gcc ctt 672
96 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
97      210      215      220
99 aaa aac aat gca tgc aca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
100 Lys Asn Asn Ala Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly
101 225      230      235      240
103 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa 768
104 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu *
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110 <211> LENGTH: 255
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112 <213> ORGANISM: H. pylori
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118      20      25      30
119 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
120      35      40      45
121 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu
122      50      55      60
123 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
124 65      70      75      80
125 Met Gln Lys Tyr Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser

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126      85      90      95
127 Ile Leu Ala Ile Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu
128      100      105      110
129 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
130      115      120      125
131 Leu Lys Gln Gln Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu
132      130      135      140
133 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
134 145      150      155      160
135 Thr Cys Met His Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val
136      165      170      175
137 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
138      180      185      190
139 Gly Tyr Phe Met Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
140      195      200      205
141 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
142      210      215      220
143 Lys Asn Asn Ala Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly
144 225      230      235      240
145 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
146      245      250      255
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154 <220> FEATURE:
155 <221> NAME/KEY: CDS
156 <222> LOCATION: (1)...(768)
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161 1 5 10 15
163 aaa agc ctt tta aaa gcg caa ttg ttt gat gaa atc atc tat tat ggc 96
164 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
165 20 25 30
167 gat agc gct aga gtg cct tat ggc act aa'a gac ccc act acg atc aag 144
168 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
169 35 40 45
171 caa ttt ggc tta gag gct ttg gat ttt ttc aaa cca cac cag att gaa 192
172 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
173 50 55 60
175 tta ttg att gtg gca tgc aac acc gca agc gct ctg gct tta gaa gag 240
176 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
177 65 70 75 80
179 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
180 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
181 85 90 95
183 att tta gcg atc aag caa caa gtg aaa gat aaa aac gcc cct att tta 336
184 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu

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187 gtg cta ggg aca aaa gcg acg att caa tcc aac gct tat gac aac gcc 384
188 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
189          115          120          125
191 ctg aaa caa caa ggc tat ttg aat gtt tcg cat tta gcc act tct ctt 432
192 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
193          130          135          140
195 ttt gtg cct ttg att gaa gaa agt att tta gag ggc gaa ttg tta gag 480
196 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
197 145          150          155          160
199 act tgc atg cgt tat tat ttc act ccc tta aag att tta cct gaa gtg 528
200 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
201          165          170          175
203 att att tta ggt tgc acg cat ttt ccc ttg att gct caa aaa att gag 576
204 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
205          180          185          190
207 ggc tat ttc atg gag cat ttt gcc ctt cca acg ccc ccc cta ctc atc 624
208 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
209          195          200          205
211 cat tcg ggc gat gct att gta gaa tat ttg cag caa aaa tac gcc ctt 672
212 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
213          210          215          220
215 aaa aac aat gca cac gca ttc cct aaa gtg gaa ttt cat gcg agc ggc 720
216 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
217 225          230          235          240
219 gat gtg atc tgg cta gaa aga caa gct aaa gaa tgg ctc aaa ttg taa 768
220 Asp Val Ile Trp Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu *
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226 <211> LENGTH: 255
227 <212> TYPE: PRT
228 <213> ORGANISM: H. pylori
230 <400> SEQUENCE: 4
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234          20          25          30
235 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
236          35          40          45
237 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
238          50          55          60
239 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
240 65          70          75          80
241 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
242          85          90          95
243 Ile Leu Ala Ile Lys Gln Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
244          100          105          110
245 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
246          115          120          125

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247 Leu Lys Gln Gln Gly Tyr Leu Asn Val Ser His Leu Ala Thr Ser Leu
248      130      135      140
249 Phe Val Pro Leu Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu
250 145      150      155      160
251 Thr Cys Met Arg Tyr Tyr Phe Thr Pro Leu Lys Ile Leu Pro Glu Val
252      165      170      175
253 Ile Ile Leu Gly Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu
254      180      185      190
255 Gly Tyr Phe Met Glu His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile
256      195      200      205
257 His Ser Gly Asp Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu
258      210      215      220
259 Lys Asn Asn Ala His Ala Phe Pro Lys Val Glu Phe His Ala Ser Gly
260 225      230      235      240
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262      245      250      255
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271 <221> NAME/KEY: CDS
272 <222> LOCATION: (1)...(768)
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277 1      5      10      15
279 aaa agc ctt tta aaa gcg caa tta ttt gat gaa atc atc tat tat ggc 96
280 Lys Ser Leu Leu Lys Ala Gln Leu Phe Asp Glu Ile Ile Tyr Tyr Gly
281      20      25      30
283 gat agc gct aga gtg cct tat ggc act aaa gac ccc act acg atc aag 144
284 Asp Ser Ala Arg Val Pro Tyr Gly Thr Lys Asp Pro Thr Thr Ile Lys
285      35      40      45
287 caa ttt ggc tta gag gct ttg gat ttt ttc aaa ccg cac cag att gaa 192
288 Gln Phe Gly Leu Glu Ala Leu Asp Phe Phe Lys Pro His Gln Ile Glu
289      50      55      60
291 tta ttg att gtg gca tgc aac aca gcg agc gct cta gct tta gaa gag 240
292 Leu Leu Ile Val Ala Cys Asn Thr Ala Ser Ala Leu Ala Leu Glu Glu
293 65      70      75      80
295 atg caa aag cat tcc aaa atc cct att gtg ggc gtg att gag cca agc 288
296 Met Gln Lys His Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser
297      85      90      95
299 att tta gcg atc aag cga caa gta aaa gat aaa aac gcc cct att tta 336
300 Ile Leu Ala Ile Lys Arg Gln Val Lys Asp Lys Asn Ala Pro Ile Leu
301      100      105      110
303 gtg cta ggg aca aaa gcg acg atc caa tcc aac gct tat gac aat gcc 384
304 Val Leu Gly Thr Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala
305      115      120      125
307 ctg aaa caa caa ggc tat ttg aat gtt tgc cat tta gcc act tct ctt 432

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